## SEQUENCE LISTING

<110> KISHIMOTO, Tadamitsu
 NAGASAWA, Takashi
 TACHIBANA, Kazunobu
 IIZASA, Hisashi
 YOSHIDA, Nobuaki
 NAKAJIMA, Toshihiro
 YOSHIE, Osamu

<120> NOVEL MOUSE CXC CHEMOKINE RECEPTOR

<130> 1422-386P

<140>

<141>

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 1877

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (120)..(1196)

<400> 1

ccatcctaat acgactcact atagggctcg agcggccgcc cgggcaggtg caggtagcag 60

tgaccetetg aggegtttgg tgeteeggta accaecaegg etgtagageg agtgttgee 119

atg gaa ccg atc agt gtg agt ata tac act tct gat aac tac tct gaa 167 Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu

1 5 10 15

gaa gtg ggg tet gga gae tat gae tee aac aag gaa eee tge tte egg 215 Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg 20 25 30

gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc 263
Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe
35 40 45

atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc 311

Ile	Ile 50	Phe	Leu	Thr	Gly	Ile 55	Val	Gly	Asn	Gly	Leu 60	Val	Ile	Leu	Val	
_			_			cta Leu										359
						ctc Leu										407
						gac Asp										455
_	_					act Thr										503
						gac Asp 135										551
						aaa Lys										599
	_				_	ctc Leu		_								647
						gac Asp										695
	-	_				gat Asp	_									743
_			_			ctc Leu 215		_				_				791
		-				tct Ser										839
aag	cgc	aag	gcc	ctc	aag	acg	aca	gtc	atc	ctc	atc	cta	gct	ttc	ttt	887

Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe 245 250 255	
gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc ttc atc 935 Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile 260 265 270	
ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc att gtg cac 983 Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His 275 280 285	
aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc cac tgt tgc ctg  Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu  290 295 300	1
aac ccc atc ctc tat gcc ttc ctc ggg gcc aag ttc aaa agc tct gcc  Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala 305 310 315 320	9
cag cat gca ctc aac tcc atg agc aga ggc tcc agc ctc aag atc ctt  Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu  325  330  335	7
tcc aaa gga aag cgg ggt gga cac tct tcc gtc tcc acg gag tca gaa 117. Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu 340 345 350	5
tcc tcc agt ttt cac tcc agc taacccttat gcaaagactt atataatata	6
tatatatata tgataaagaa cttttttatg ttacacattt tccagatata agagactgac 128	6
cagtcttgta cagtttttt tttttttaa ttgactgttg ggagtttatg ttcctctagt 134	6
ttttgtgagg tttgacttaa tttatataaa tattgttttt tgtttgtttc atgtgaatga 140	6
gcgtctaggc aggacctgtg gccaagttct tagtagctgt ttatctgtgt gtaggactgt 146	6
agaactgtag aggaagaaac tgaacattcc agaatgtgtg gtaaattgaa taaagctagc 152	
agaactgtag aggaagaaac tgaacattcc agaatgtgtg gtaaattgaa taaagctagc 152 cgtgatcctc agctgttgct gcataatctc ttcattccga ggagcacccc acccccaccc 158	6
	6 6
cgtgatcctc agctgttgct gcataatctc ttcattccga ggagcacccc acccccaccc 158	6 6

<210> 2

<211> 359

<212> PRT

<213> Mus sp.

<400> 2

Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu

1 5 10 15

Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg
20 25 30

Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe 35 40 45

Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val 50 55 60

Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu 65 70 75 80

His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp

85 90 95

Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys
100 105 110

Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile 115 120 125

Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr 130 135 140

Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val 145 150 155 160

Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe 165 170 175

Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile 180 185 190 Cys Asp Arg Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser <210> 3 <211> 690

<210> 3
<211> 690
<212> DNA
<213> Mus sp.
<220>
<221> CDS
<222> (1)..(690)

<400> 3

ctg cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc 45
Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe
1 5 10 15

	_	-	-								ggg Gly			96
_	-	_									tac Tyr			144
	_	_									gcc Ala 60			192
		-						_	_	_	gaa Glu			240
		_				-					ata Ile			288
	-	-	-	_	_		-				Gly ggg			336
	_	-	_				-				atg Met			384
	_										ggc Gly 140			432
	-		_								cac His			480
_											ctc Leu			528
	_	_		_							agc Ser			576
											ttc Phe			624

	_					aca Thr 215	-	_								672
_			atc Ile													690
<212	L> 23 2> PE		o.													
<400	)> 4															
		Leu	Ser	Val 5	Ala	Asp	Leu	Leu	Phe 10	Val	Ile	Thr	Leu	Pro 15	Phe	
Trp	Ala	Val	Asp 20	Ala	Met	Ala	Asp	Trp 25	Tyr	Phe	Gly	Lys	Phe 30	Leu	Cys	
Lys	Ala	Val 35	His	Ile	Ile	Tyr	Thr 40	Val	Asn	Leu	Tyr	Ser 45	Ser	Val	Leu	
Ile	Leu 50	Ala	Phe	Ile	Ser	Leu 55	Asp	Arg	Tyr	Leu	Ala 60	Ile	Val	His	Ala	
Thr 65	Asn	Ser	Gln	Arg	Pro 70	Arg	Lys	Leu	Leu	Ala 75	Glu	Lys	Ala	Val	Tyr 80	
Val	Gly	Val	Trp	Ile 85	Pro	Ala	Leu	Leu	Leu 90	Thr	Ile	Pro	Asp	Phe 95	Ile	
Phe	Ala	Asp	Val 100	Ser	Gln	Gly	Asp	Ile 105	Ser	Gln	Gly	Asp	Asp 110	Arg	Tyr	
Ile	Cys	Asp 115	Arg	Leu	Tyr	Pro	Asp 120	Ser	Leu	Trp	Met	Val 125	Val	Phe	Gln	
Phe	Gln 130	His	Ile	Met	Val	Gly 135	Leu	Ile	Leu	Pro	Gly 140	Ile	Val	Ile	Leu	
Ser 145	Cys	Tyr	Cys	Ile	Ile 150	Ile	Ser	Lys	Leu	Ser 155	His	Ser	Lys	Gly	His 160	

Gln Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe

Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser Phe 185 180 Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser Ile Val 205 195 200 His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys 220 215 Leu Asn Pro Ile Leu Tyr 230 225 <210> 5 <211> 685 <212> DNA <213> Mus sp. <220> <221> CDS <222> (120)..(683) <400> 5 ccatcctaat acgactcact atagggctcg agcggccgcc cgggcaggtg caggtagcag 60 tgaccetctg aggegtttgg tgctccggta accaccacgg ctgtagagcg agtgttgcc atg gaa ccg atc agt gtg agt ata tac act tct gat aac tac tct gaa 167 Met Glu Pro Ile Ser Val Ser Ile Tyr Thr Ser Asp Asn Tyr Ser Glu 1 5 10 15 215 gaa gtg ggg tot gga gac tat gac toc aac aag gaa coc tgc ttc cgg Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys Phe Arg 20 gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc atc tac ttc 263 Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr Ile Tyr Phe 35 40 45 atc atc ttc ttg act ggc ata gtc ggc aat gga ttg gtg atc ctg gtc 311 Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val 50 55 359 atg ggt tac cag aag aag cta agg agc atg acg gac aag tac cgg ctg Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu 70 75 65

cac ctg tca gtg gct gac ctc ctc ttt gtc atc aca ctc ccc ttc tgg

407

	His	Leu	Ser	Val	Ala 85	Asp	Leu	Leu	Phe	Val 90	Ile	Thr	Leu	Pro	Phe 95	Trp		
<b>.</b>	-												ttt Phe				455	
	_												agc Ser 125				503	
													gtc Val				551	
·													gca Ala				599	
		_											gac Asp				647	
	_								agt Ser 185				ga				685	
	<212	l> 18 2> PF		o.														
		)> 6 Glu	Pro	Ile	Ser 5	Val	Ser	Ile	Tyr	Thr 10		Asp	Asn	Tyr	Ser 15	Glu		
	Glu	Val	Gly	Ser 20	Gly	Asp	Tyr	Asp	Ser 25	Asn	Lys	Glu	Pro	Cys 30	Phe	Arg		
	Asp	Glu	Asn 35	Val	His	Phe	Asn	Arg 40	Ile	Phe	Leu	Pro	Thr 45	Ile	Tyr	Phe		
	Ile	Ile 50	Phe	Leu	Thr	Gly	Ile 55	Val	Gly	Asn	Gly	Leu 60	Val	Ile	Leu	Val		
	Met 65	Gly	Tyr	Gln	Lys	Lys 70	Leu	Arg	Ser	Met	Thr 75	Asp	Lys	Tyr	Arg	Leu 80		

90 Ala Val Asp Ala Met Ala Asp Trp Tyr Phe Gly Lys Phe Leu Cys Lys 100 105 Ala Val His Ile Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile 120 Leu Ala Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr 135 140 Asn Ser Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Ala Val Tyr Val 155 145 150 160 Gly Val Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe 165 170 175 Ala Asp Val Ser Gln Gly Asp Ile Ser Gln Gly Asp 180 185 <210> 7 <211> 1694 <212> DNA <213> Mus sp. <220> <221> CDS <222> (1)..(1056) <400> 7 ata tac act tct qat aac tac tct qaa qaa gtg ggg tct gga gac tat Ile Tyr Thr Ser Asp Asn Tyr Ser Glu Glu Val Gly Ser Gly Asp Tyr 5 10 15 1 gac tcc aac aag gaa ccc tgc ttc cgg gat gaa aac gtc cat ttc aat 96 Asp Ser Asn Lys Glu Pro Cys Phe Arg Asp Glu Asn Val His Phe Asn 20 25 agg atc ttc ctg ccc acc atc tac ttc atc ttc ttg act ggc ata Arg Ile Phe Leu Pro Thr Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile 35 40 45 gtc ggc aat gga ttg gtg atc ctg gtc atg ggt tac cag aag aag cta 192 Val Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu 50 55

His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp

	_	_	acg Thr								240
		-	atc Ile				_				288
			ggg Gly 100								336
			tac Tyr								384
			gcc Ala								432
			gaa Glu								480
	-		ata Ile								528
			ggg Gly 180								576
			atg Met								624
	-		ggc Gly	_			-				672
_	_		cac His								720
	_		ctc Leu		-						768

	-			tg gga gtc ato eu Gly Val Ile 270	e Lys Gln	816
,,	Phe Glu	-	l His Lys T	gg atc tcc atc rp Ile Ser Ile 285	· · · · · · · · ·	864
-		-		cc atc ctc tat ro Ile Leu Tyn 300		912
	Lys Phe		r Ala Gln H	at gca ctc aad is Ala Leu Asn 15		960
	_	-		aa gga aag cgg ys Gly Lys Arg		1008
	-			cc agt ttt cac er Ser Phe His 350	s Ser Ser	1056
taacccttat	gcaaagact	t atataata	ta tatatata	ta tgataaagaa	cttttttatg	1116
ttacacattt	tccagatat	a agagactg	ac cagtcttg	ta cagtttttt	tttttttaa	1176
ttgactgttg	ggagtttat	g ttcctcta	gt ttttgtga	gg tttgacttaa	tttatataaa	1236
tattgttttt	tgtttgttt	c atgtgaat	ga gcgtctag	gc aggacctgtg	gccaagttct	1296
tagtagctgt	ttatctgtg	t gtaggact	gt agaactgt	ag aggaagaaac	tgaacattcc	1356
agaatgtgtg	gtaaattga	a taaagcta	gc cgtgatcc	tc agctgttgct	gcataatctc	1416
ttcattccga	ggagcaccc	c acccccac	cc ccacccc	ac cccattctta	aattgtttgg	1476
ttatgctgtg	tgatggttt	g tttggttt	tt ttttgttg	tt gttgttgttt	tttttttctg	1536
taaaagatgg	cacttaaaa	c caaageet	ga aatggtgg	ta gaaatgctgg	ggttttttt	1596
gtttgtttgt	tttttcagt	t ttcaagag	ta gattgact	tc agtccctaca	aatgtacagt	1656
cttgtattac	attgttaat	a aaagtcaa	tg ataaactt			1694

<210> 8 <211> 352

<212> PRT

<213> Mus sp.

<400> 8

Asp Ser Asn Lys Glu Pro Cys Phe Arg Asp Glu Asn Val His Phe Asn 20 25 30

Arg Ile Phe Leu Pro Thr Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile 35 40 45

Val Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu 50 55 60

Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu 65 70 75 80

Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp 85 90 95

Trp Tyr Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr
100 105 110

Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp 115 120 125

Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys 130 135 140

Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser Gln Gly Asp 165 170 175

Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg Leu Tyr Pro Asp 180 185 190

Ser Leu Trp Met Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu 195 200 205

Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser 210 215 220

Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr 225 230 235 240

Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr 245 250 255

Val Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Gly Val Ile Lys Gln 260 265 270

Gly Cys Asp Phe Glu Ser Ile Val His Lys Trp Ile Ser Ile Thr Glu 275 280 285

Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe 290 295 300

Leu Gly Ala Lys Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met 305 310 315 320

Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly 325 330 335

His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser 340 345 350

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<220>

<221> modified base

<222> (13)

<223> i

<220>

<221> modified base

<222> (15)

<223> i

<400> 9

ctsmgtttgk cmntnkcyga

20

```
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<220>
<221> modified_base
<222> (8)..(9)
<223> i
<220>
<221> modified_base
<222> (17)
<223> i
<400> 10
                                                                    26
tagaksanng grttsanrca rcagtg
<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 11
                                                                    25
tcatcccct gactgatgtc cccct
<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic DNA
<400> 12
                                                                    27
ccatcctaat acgactcact atagggc
<210> 13
<211> 30
<212> DNA
```

<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic DNA	
<400> 13	
cgcgtcgacc acaacatgct gtccacatca	30
<210> 14	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
4000	
<220>	
<223> Description of Artificial Sequence: Synthetic DNA	
<400> 14	
cgctctagat tataaaccag ccgagacttc	30
<210> 15	
<211> 29	
<211> 25 <212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic DNA	
<400> 15	
<400> 15 cgcgtcgacg ttaccatgga ggggatcag	29
cycyccyacy tracearyya yygyareay	
<210> 16	
<211> 32	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: Synthetic DNA	
<400> 16	32
cgcgcggccg cttagctgga gtgaaaactt ga	JL
<210> 17	
<211> 27	

<212> DNA

<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Synthetic DNA	
<400>	17	
tagcgg	geege gttgeeatgg aaccgat	27
<210>	18	
<211>	27	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Synthetic DNA	
<400>	18	
gcgtc	gacta agggttagct ggagtga	27
<210>	19	
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Synthetic DNA	
<400>	19	
ctgcad	eetgt cagtggetga	20
<210>		
<211>		
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Description of Artificial Sequence: Synthetic DNA	
<400>	20	
tagat	gaggg ggattgagac aacagtg	27
<210>	21	
<211>	1776	
<212>	DNA	

	l> CI		. (325	i)												
	)> 2: gģtgt		ctto	jctgt	ic ca	agcto	etgca	a gco	etecç	jgcg	cgco	cctco	ccg (	ccac	egec	58
	-	_	_	-	-									gcg Ala 15		106
_		-												ccc Pro		154
				_										ctg Leu		202
														ctg Leu		250
														atc Ile		298
		-	gag Glu						taaq	gcaca	aac a	agcco	caaa	gg		345
actt	tcca	agt a	agaco	cccc	ga go	gaago	gctga	a cat	ccgt	ggg	agat	gcaa	agg	gcagt	ggtgg	405
gga	ggag	ggc (	ctgaa	accct	ig go	ccago	gatgo	g cci	ggcg	ggac	agca	actga	act	ggggt	catgc	465
taaq	ggtt	tgc (	cagca	ataaa	ag ad	cacto	ccgc	c ata	agcat	tatg	gtad	cgata	att	gcago	cttata	525
ttca	atcc	ctg (	ccct	egeed	eg to	gcaca	aatg	g ago	ctttt	tata	acto	ggggt	ttt	ttcta	aaggaa	585
ttgt	tatta	acc (	ctaad	ccagt	it ag	gctto	catco	c cca	attct	cct	cato	ectca	atc	ttcat	tttaa	645
aaaq	gcag	tga †	ttact	tcaa	ag go	gctgt	catto	c agt	ttg	cttt	gga	gctt	ctc	tttg	ccctgg	705
ggc	ctct	ggg (	cacaç	gttat	a ga	acggt	ggct	t tt	gcag	ggag	ccci	taga	gag	aaac	cttcca	765

<213> Mus musculus

ccagagcaga gtccgaggaa cgctgcaggg cttgtcctgc agggggggct cctcgacaga 825

tgccttgtcc tgagtcaaca caagatccgg cagagggagg ctcctttatc cagttcagtg 885 ccagggtcgg gaagetteet ttagaagtga teeetgaage tgtgetcaga gaeeetttee 945 tagecqttcc tgctctctqc ttgcctccaa acgcatgctt catctgactt ccgcttctca 1005 cctctqtaqc ctqacqqacc aatqctqcaa tqqaaqgqaq qaqaqtqatq tqqqqtqccc 1065 cetecetete tteeetttge ttteetetea ettgggeeet ttgtgagatt tttetttgge 1125 ctcctgtaga atggagccag accatcctgg ataatgtgag aacatgccta gatttaccca 1185 caaaacacaa gtctgagaat taatcataaa cggaagttta aatgaggatt tggactttgg 1245 taattgtccc tgagtcctat atatttcaac agtggctcta tgggctctga tcgaatatca 1305 gtgatgaaaa taataataat aataataata acgaataagc cagaatcttg ccatgaagcc 1365 acagtgggga ttctgggttc caatcagaaa tggagacaag ataaaacttg catacattct 1425 tacgatcaca gacggccctg gtggtttttg gtaactattt acaaggcatt tttttacata 1485 tatttttgtg cactttttat gtttctttgg aagacaaatg tatttcagaa tatatttgta 1545 gtcaattcat atatttgaag tggagccata gtaatgccag tagatatctc tatgatcttg 1605 agctactggc aacttgtaaa gaaatatata tgacatataa atgtattgta gctttccggt 1665 gtcagccacg gtgtattttt ccacttggaa tgaaattgta tcaactgtga cattatatgc 1725 1776 actaqcaata aaatgctaat tgtttcatqc tgtaaaaaaa aaaaaaaaaa a

<210> 22

<211> 89

<212> PRT

<213> Mus musculus

<400> 22

Met Asp Ala Lys Val Val Ala Val Leu Ala Leu Val Leu Ala Ala Leu 1 5 10 15

Cys Ile Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
20 25 30

Arg Phe Phe Glu Ser His Ile Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45

Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys 50 55 60

Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln 65 70 75 80

Glu Tyr Leu Glu Lys Ala Leu Asn Lys 85